N-TERMINAL

P26h	MK	LN	FS	XL	RA	LV	TG	AG	KG	IG	IG	XD	TA	KA	L
Adipsin	--	--	--	G-	--	--	--	--	--	--	--	R-	-V	--	-

NCS FRAGMENT

P26h	XA	TE	KA	LG	XI	GP	VX	XL	VN	NA	AL	XX	XQ
Adipsin	D-	--	--	--	G-	--	-D	L-	--	--	--	VM	I-

CNBr fragment

P26h	LY	PY	KX	RV	N
Adipsin	-G	-H	-I	--	-

Fig. 1

SUBSTITUTE SHEET (RULE 26)

09/21 9053

PCT/CA99/00437

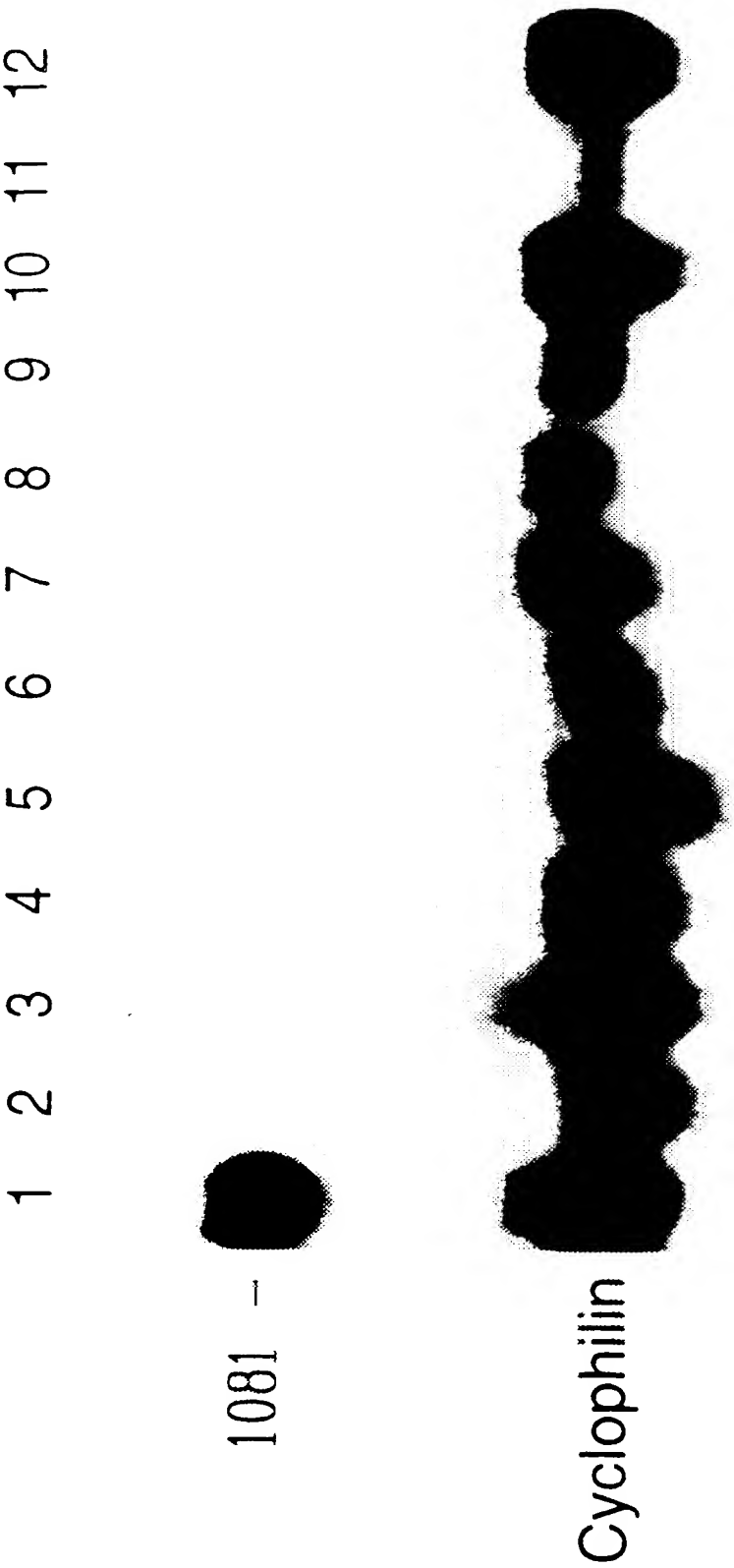

Fig. 2

SUBSTITUTE SHEET (RULE 26)

```
GTCCCTGGAGGTTGGCTGTAGGATTCAGGTGGCTTGCTCAGGCTGGG      47
ATCAAGGACACAGTGAGCAGATCAACCTTAACCTCAGCCCCTCCC        92
CTCGCCACAGGAGGACACTGGTGTCAGCAGC ATG AAG CTG AAT      135
                                 M   K   L   N        4

TTC ACT GGT CTC AGG GCT CTG GTG ACC GGG GCA GGG AGA GGG   177
 F   T   G   L   R   A   L   V   T   G   A   G   R   G    18

ATT GGG CGA GGC ACT GCG AAA GCC CTG CAT GCC TCA GGA GCC   219
 I   G   R   G   T   A   K   A   L   H   A   S   G   A    32

AAA GTG GTG GCC GTG TCA CTC ATC AAC GAA GAC CTG GTC AGC   261
 K   V   V   A   V   S   L   I   N   E   D   L   V   S    46

CTG GCC AAA GAG TGT CCG GGC ATA GAG CCT GTG TGT GTG GAC   303
 L   A   K   E   C   P   G   I   E   P   V   C   V   D    60

CTG GGT GAC TGG GAG GCC ACA GAG AAG GCA CTG GGC CGT ATT   345
 L   G   D   W   E   A   T   E   K   A   L   G   R   I    74

GGC CCC GTG GAC CTG CTG GTG AAC AAT GCG GCG GTG GCG CTA   387
 G   P   V   D   L   L   V   N   N   A   A   V   A   L    88
```

FIG 3A

SUBSTITUTE SHEET (RULE 26)

```
GTG CAG CCT TTC ATA CAG TCT ACC AAG GAG GTC TTT GAC AGG    429
 V   Q   P   F   I   Q   S   T   K   E   V   F   D   R    102

TCC TTC AAT GTG AAT GTG CGC TCT GTG CTG CAA GTG TCC CAG    471
 S   F   N   V   N   V   R   S   V   L   Q   V   S   Q    116

ATG GTA GCC AAG GGC ATG ATT AAC CGT GGA GTG GCA GGA TCC    513
 M   V   A   K   G   M   I   N   R   G   V   A   G   S    130

ATT GTC AAC ATC TCC AGC ATG GTG GCC TAT GTC ACC TTC CCT    555
 I   V   N   I   S   S   M   V   A   Y   V   T   F   P    144

GGT CTG GCC ACG TAC AGC TCC ACC AAG GGT GCT ATA ACC ATG    597
 G   L   A   T   Y   S   S   T   K   G   A   I   T   M    158

CTG ACC AAA GCC ATG GCC ATG GAG CTG GGA CCA TAC AAG ATC    639
 L   T   K   A   M   A   M   E   L   G   P   Y   K   I    172

CGG GTG AAC TCT GTA AAC CCT ACC GTG GTG CTG ACT GAC ATG    681
 R   V   N   S   V   N   P   T   V   V   L   T   D   M    186

GGC AAG AAA GTC TCT GCA GAC CCG GAA TTT GCC AAG AAG CTC    723
 G   K   K   V   S   A   D   P   E   F   A   K   K   L    200
```

FIG - 3B

```
AAG GAG CGC CAC CCA CTG AGG AAG TTC GCA GAG GTG GAG GAC  765
 K   E   R   H   P   L   R   K   F   A   E   V   E   D   214

GTG GTC AAC AGC ATC CTC TTC CTG CTC AGC GAC AGC AGC GCC  807
 V   V   N   S   I   L   F   L   L   S   D   S   S   A   228

TCT ACC AGC GGC TCT GGC ATC CTG GTG GAC GCT GGT TAC CTG  849
 S   T   S   G   S   G   I   L   V   D   A   G   Y   L   242

GCC TCC TAG     ACGGCCCAGGTGCAGGGGACTCCTGGAGACTTCC       892
 A   S  Amber                                           244

CTGGCCTCACCCTTACATCAAGACCCCGCCTTCAACCCAACCCAATAAT       941
TTTGTTCGAATCCTGTAGAGCCCCACCCCACACACATCCATCCCCAACT       990
TTAGACTCCGGGATCCCGCCATTCCATACCAGCTATGCTGAGATAATT        1038
TGATTAAATAAGTATCCCAAACCACAAAAAAAAAAAAAAAAAA             1081
```

Fig. 3C

P26h	MK LN FT GL RA LV TG AG RG IG RG TA KA LH AS GA KV VA VS LI NE DL VS LA KE	50
Adipsin	-- -- -S -- -- -- -- -- -- -- -D -V -- -- -- -- -- -- -T RT -S -- -- -- --	50
C.Reductase	-Q M- -S -- -- -- -- -- K- -- -D -V -- -- V- -- R- -- -T RT -G -- -- -S Q-	50
P26h	CP GI EP VC VD LG DWEA TE KA LG RI GP VD LL VN NA AV AL VQ PF IQ ST KE VF	100
Adipsin	-- -- -- -- -- -- -- D- -- -- -- G- -- -- -- -- -- -- -L VI M- -- LE V- -- A-	100
C.Reductase	-- -- -- -- -- -- -- -- -- -- R- -- GV -- -- -- -- -- -- -- -- M- - LD T- -- --	100
P26h	DR SF NV NV RS VL QV SQ MV AK GM IN RG VA GS IV NI SS MV AY VT FP GL AT YS	150
Adipsin	-- -- S- -L -- -F -- -- -- -R D- -- -- -P -- -- -V -- -- -H -- -- N- I- --	150
C.Reductase	-- -- -- -L -- -F -- -- I- -R S- -E -- -P -- - -V -- -- SH -- Y- -- -A –	150

Fig 4A

P26h	ST	KG	AI	TM	LT	KA	MA	ME	LG	PY	KI	RV	NS	VN	PT	VV	LT	DM	GK	KV	SA	DP	EF	AK	KL	200
Adipsin	--	--	-M	--	--	-	--	--	--	-H	--	--	--	--	--	--	--	--	--	--	--	--	--	-R	--	200
C.Reductase	--	--	-M	--	--	-S	--	--	--	-H	--	--	--	--	--	--	--	A-	-R	S-	TS	--	-L	-R	--	200

P26h	KE	RH	PL	RK	FA	EV	ED	VV	NS	IL	FL	LS	DS	SA	ST	SG	SG	I L	VD	AG	YL	AS	244
Adipsin	--	--	--	--	--	--	--	--	--	--	--	--	-R	--	--	--	G-	--	--	--	--	--	244
C.Reductase	--	--	-M	--	--	--	--	--	--	--	--	--	-R	--	--	--	-S	-F	--	--	--	--	244

FIG. 4B

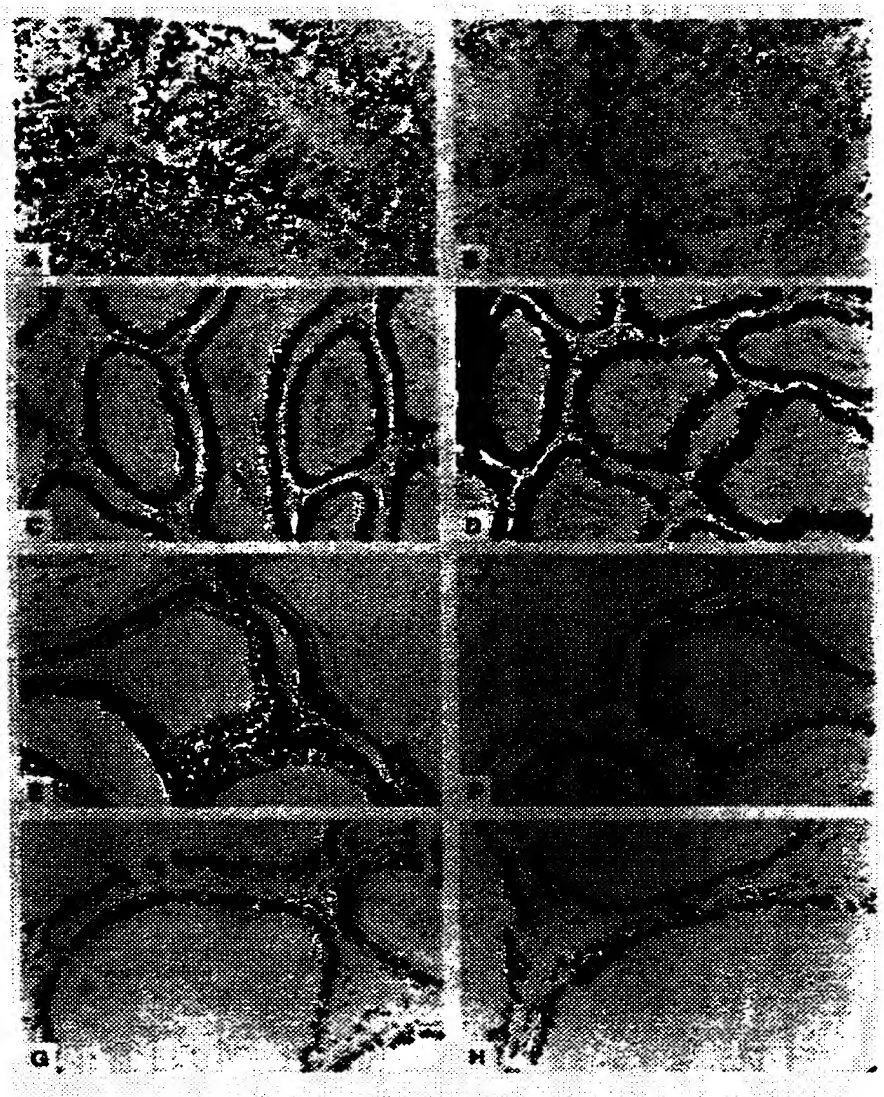

FIG. 5

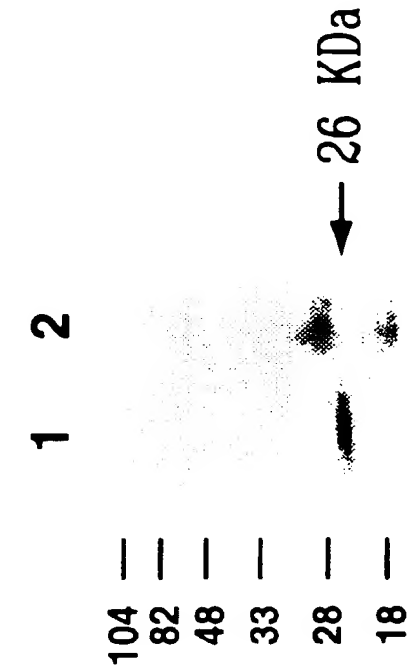

Fig-6B

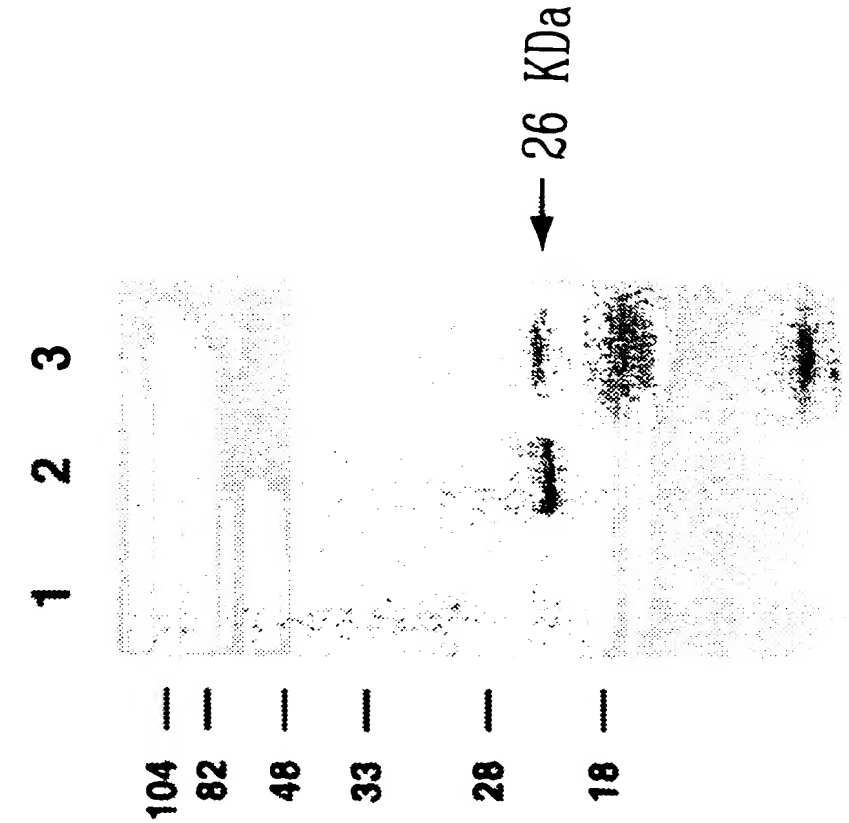

Fig-6A

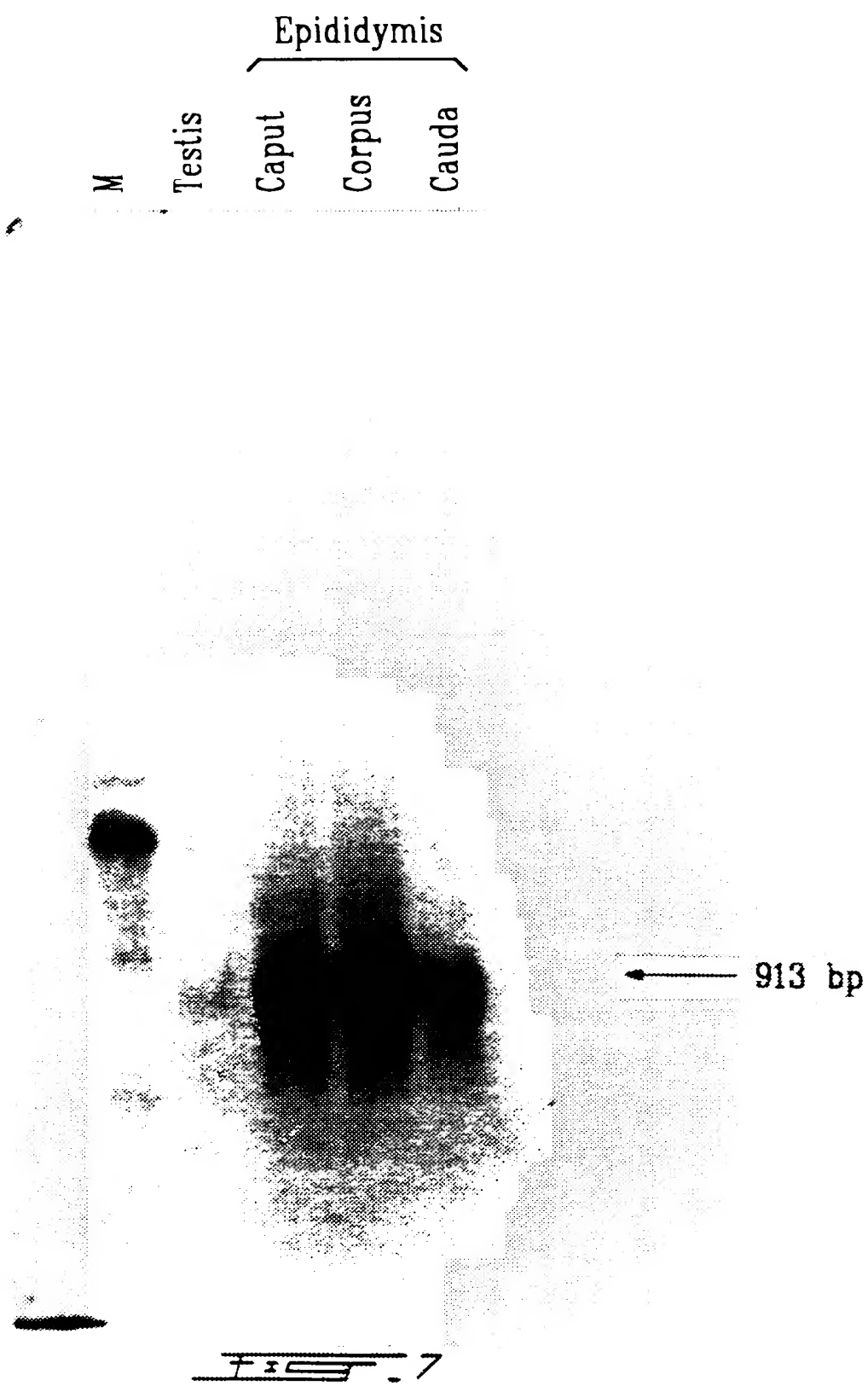

Fig. 7

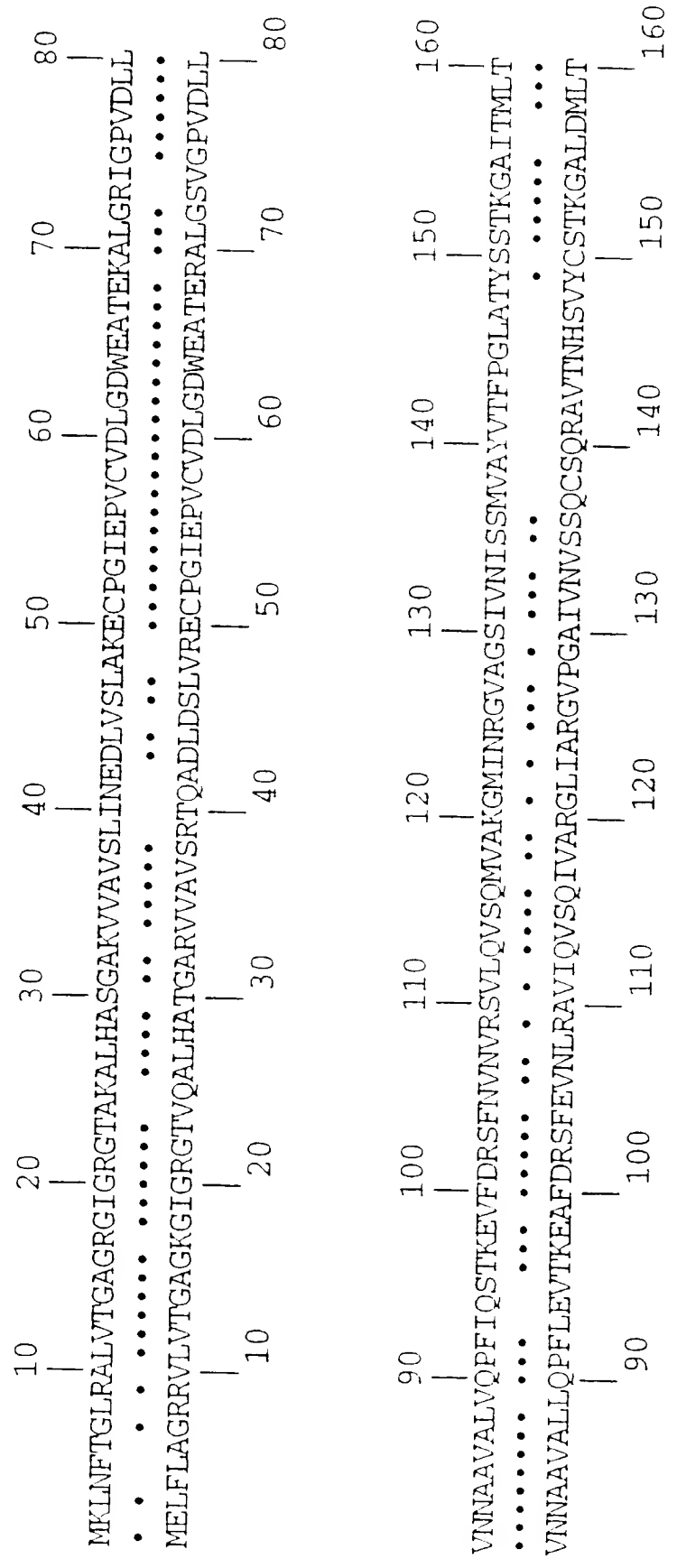
10 20 30 40 50 60 70 80
MKLNFTGLRALVTGAGRGIGRGTAKALHASGAKVVAVSLINEDLVSLAKECPGIEPVCVDLGDWEATEKALGRIGPVDLL
MELFLAGRRVLVTGAGKGIGRGTVQALHATGARVVAVSRTQADLDSLVRECPGIEPVCVDLGDWEATERALGSVGPVDLL
10 20 30 40 50 60 70 80
90 100 110 120 130 140 150 160
VNNAAVALVQPFIQSTKEVFDRSFNVNVRSVLQVSQMVAKGMINRGVAGSIVNISSMVAYVTFPGLATYSSTKGAITMLT
VNNAAVALLQPFLEVTKEAFDRSFEVNLRAVIQVSQIVARGLIARGVPGAIVNVSSQCSQRAVTNHSVYCSTKGALDMLT
90 100 110 120 130 140 150 160

FIG-8A

```
                170       180       190       200       210       220       230       240
                  |         |         |         |         |         |         |         |
YLAS  KAMAMELGPYKIRVNSVNPTVVLTDMGKKVSADPEFAKKLKERHPLRKFAEVEDVVNSILFLLSDSSASTSGSGILVDAG
  .   . .. .... ..... ...... . ..     ..  ..    . .. ...... ... ....... .  . ..   .  .
FWAC. KVMALELGPHKIRVNAVNPTVVMTSMGQATWSDPHKAKTMLNRIPLGKFAEVEHVVNAILFLLSDRSGMTTGSTLPVERG
                  |         |         |         |         |         |         |         |
                170       180       190       200       210       220       230       240
```

FIG. 8B